

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- subC²
- (i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo
 - (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
 - (iii) NUMBER OF SEQUENCES: 54
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 14-FEBRUARY-1996
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 16-JANUARY-1996
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 600-1-162 CP1
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2821 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
CODING REGION: 1-2682
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCCCT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACGTCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCCTC TGCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTTG TGAAACCCGA TCCACCCTTA	720
GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTTGGGA CAGCCAAACA	780
ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960
AGTTCACCTC AAGTCTTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT	1020
AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC	1080
TCAAAACAGA TAGTTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC	1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA	1200
GGGAAGTTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT	1260
GCTGAATTAT ACGTGATCGA TGTCAATATC AATATATCAT GTGAAACTGA CGGGTACTTA	1320
ACTAAAATGA CTTGCAGATG GTCACCCAGC ACAATCCAAT CACTAGTGGG AAGCACTGTG	1380
CAGCTGAGGT ATCACAGGCG CAGCCTGTAT TGTCCTGATA GTCCATCTAT TCATCTACG	1440
TCTGAGCCCA AAAACTGCGT CTTACAGAGA GACGGCTTTT ATGAATGTGT TTTCCAGCCA	1500
ATCTTTCTAT TATCTGGCTA TACAATGTGG ATCAGGATCA ACCATTCTTT AGGTTCACTT	1560
GA CTCGCCAC CAACGTGTGT CCTTCCTGAC TCCGTAGTAA AACCCTACC TCCATCTAAC	1620
GTAAAAGCAG AGATTACTGT AAACACTGGA TTATTGAAAG TATCTTGGGA AAAGCCAGTC	1680
TTTCCGGAGA ATAACCTTCA ATTCCAGATT CGATATGGCT TAAGTGAAAA AGAAATACAA	1740

TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTCTAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTTCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCTGTGGA	CAGAACCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCCT	GAGCAGCAGC	TGTGTCATCC	TTTCTTGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTTAC	CCAGTATTTA	TGGAAGGAGT	TGGAAAACCA	2460
AAGATAATTA	ATGGTTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520
TATGTCATTG	TACCCATAAT	TATTTCTCT	TGTGTCCTAC	TGCTCGGAAC	ACTGTTAATT	2580
TCACACCAGA	GAATGAAAAA	GTTGTTTTGG	GACGATGTTT	CAAACCCCAA	GAATTGTTCC	2640
TGGGCACAAG	GACTGAATTT	CCAAAAGAGA	ACGGACACTC	TTTGAAGTCT	CTCATGACCA	2700
CTACAGATGA	ACCCAATCTA	CCAACCTCCC	AACAGTCCAT	ACAATATTAG	AAGATGTTTA	2760
CATTTGGATG	GAGGGAAACA	ACCCTAAACT	ATGGTTTGAA	TGACTAAGAA	ATAACATTTG	2820
A						2821

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu
1				5					10					15	

Tyr	Val	Ile	Ala 20	Ala	Leu	Asn	Leu	Ala 25	Tyr	Pro	Ile	Ser	Pro 30	Trp	Lys
Phe	Lys	Leu 35	Phe	Cys	Gly	Pro	Pro 40	Asn	Thr	Thr	Asp	Asp 45	Ser	Phe	Leu
Ser	Pro 50	Ala	Gly	Ala	Pro	Asn 55	Asn	Ala	Ser	Ala	Leu 60	Lys	Gly	Ala	Ser
Glu 65	Ala	Ile	Val	Glu	Ala 70	Lys	Phe	Asn	Ser	Ser 75	Gly	Ile	Tyr	Val	Pro 80
Glu	Leu	Ser	Lys	Thr 85	Val	Phe	His	Cys	Cys 90	Phe	Gly	Asn	Glu	Gln 95	Gly
Gln	Asn	Cys	Ser 100	Ala	Leu	Thr	Asp	Asn 105	Thr	Glu	Gly	Lys	Thr 110	Leu	Ala
Ser	Val	Val 115	Lys	Ala	Ser	Val	Phe 120	Arg	Gln	Leu	Gly	Val 125	Asn	Trp	Asp
Ile	Glu 130	Cys	Trp	Met	Lys	Gly 135	Asp	Leu	Thr	Leu	Phe 140	Ile	Cys	His	Met
Glu 145	Pro	Leu	Pro	Lys	Asn 150	Pro	Phe	Lys	Asn	Tyr 155	Asp	Ser	Lys	Val	His 160
Leu	Leu	Tyr	Asp	Leu 165	Pro	Glu	Val	Ile	Asp 170	Asp	Ser	Pro	Leu	Pro 175	Pro
Leu	Lys	Asp	Ser 180	Phe	Gln	Thr	Val	Gln 185	Cys	Asn	Cys	Ser	Leu 190	Arg	Gly
Cys	Glu	Cys 195	His	Val	Pro	Val	Pro 200	Arg	Ala	Lys	Leu	Asn 205	Tyr	Ala	Leu
Leu	Met 210	Tyr	Leu	Glu	Ile	Thr 215	Ser	Ala	Gly	Val	Ser 220	Phe	Gln	Ser	Pro
Leu 225	Met	Ser	Leu	Gln	Pro 230	Met	Leu	Val	Val	Lys 235	Pro	Asp	Pro	Pro	Leu 240
Gly	Leu	His	Met	Glu 245	Val	Thr	Asp	Asp	Gly 250	Asn	Leu	Lys	Ile	Ser 255	Trp
Asp	Ser	Gln	Thr 260	Met	Ala	Pro	Phe	Pro 265	Leu	Gln	Tyr	Gln	Val 270	Lys	Tyr
Leu	Glu	Asn 275	Ser	Thr	Ile	Val	Arg 280	Glu	Ala	Ala	Glu	Ile 285	Val	Ser	Ala
Thr	Ser 290	Leu	Leu	Val	Asp	Ser 295	Val	Leu	Pro	Gly	Ser 300	Ser	Tyr	Glu	Val
Gln 305	Val	Arg	Ser	Lys	Arg 310	Leu	Asp	Gly	Ser	Gly 315	Val	Trp	Ser	Asp	Trp 320
Ser	Ser	Pro	Gln	Val 325	Phe	Thr	Thr	Gln	Asp 330	Val	Val	Tyr	Phe	Pro 335	Pro
Lys	Ile	Leu	Thr 340	Ser	Val	Gly	Ser	Asn 345	Ala	Ser	Phe	His	Cys 350	Ile	Tyr
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg

355					360					365					
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp
370						375					380				
Arg	Val	Ser	Lys	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg
385					390					395					400
Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys
				405					410					415	
His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile
			420					425					430		
Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser
		435					440					445			
Pro	Ser	Thr	Ile	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr
	450					455					460				
His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
465					470					475					480
Ser	Glu	Pro	Lys	Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys
				485					490					495	
Val	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg
			500					505					510		
Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu
		515					520					525			
Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu
	530					535					540				
Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val
545					550					555					560
Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly
				565					570					575	
Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys
			580					585					590		
Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln
		595					600					605			
Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser
	610					615					620				
Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly
625					630					635					640
Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg
				645					650					655	
Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys
			660					665					670		
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr
		675					680					685			
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr
	690					695					700				

Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	705	710	715	720
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	725	730	735	
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	740	745	750	
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	755	760	765	
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	770	775	780	
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	785	790	795	800
Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	805	810	815	
Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	820	825	830	
Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	835	840	845	
Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	850	855	860	
Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	865	870	875	880
Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Arg	Thr	Asp	Thr	Leu	885	890				

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2914 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
CODING REGION: 1349-2845
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA GTGCCAACGG GAAGGCTTAA TTAACCTTTG GAANTGAGTC CGAAGAGTCT	60
GGAAGTNTGT AAGATGGAAG ATACTATACA AGATACTTCA GAGCTGTACA TTCTTCCAGG	120

GATGTAGGCT	AGCAGTTATT	TCATTAGTAT	ATGTCTATTT	TAGAATGGGA	AGAATTAGGA	180
AGATGAATGG	AGCCTGTGTC	TTTCACTACT	CTCCCAGGAG	GTTCCAGAAT	AGCNAAAGTG	240
TCAGCCAGAA	TTCTTGAAGT	CATAGACTGG	AGTTAGAGAT	GAACATAAGC	TCATGTTAAG	300
CCTGGGTTAC	TTCTTATCAT	CCTTAATTTT	GAAAGCTAAG	AGGGCCTAAC	CATCAAGAAC	360
GTCCTGGAGG	AAAGAATGTT	TTTAACGCCA	TTATTCAGTC	AAAGAAATTA	AGACTTGAGA	420
GAAATGCTCA	TTTCTTCTCT	CATGATGGCT	CCTTACACCT	TACTTCTACC	GTACGATCCA	480
TGNGGCCCTA	CCCACGCAGG	ATACATGCAT	CTATATGAGA	GTGTCTNCCC	CTTCTAACTC	540
AGAGACTCTT	GTTCTAGTCT	GTGNTATAAA	ATTCAGCTTG	TGGAAGCTTT	CTGAGGGGTT	600
GGCAGCATTC	AATTTTACCT	GCAATAGGTA	AAGGTAATCT	TTTGGGAAGT	GAAGAGTGTT	660
ATTAGACATT	TCAGAAAGAA	CAAACAGGAT	TGGGGCTGCT	ATGTGTTCTA	CACAGGAATC	720
TTCCATAACA	CAGAATAATT	TATGTAGATA	GAGACAAGAT	GGAAATGCCC	AGGGCCCCAA	780
AATAGCCGCT	GTTATTTGTT	AACCTTCAAG	GTTTTCTGTT	TGTTTATCTG	TTTCTTGCGC	840
AGGATCATCT	TCCAAGCACA	TCCTGGGGGA	ACAGTGGCAG	AGTCACTCGA	GTTCATGAAA	900
CTATGGTGAC	ATCTGAGCTT	CCTTG GTTCT	TCACAGAACA	TAAGCAGTTC	CTTTGCTTGC	960
TTGTTAGATG	AGAAAAC TTC	CTTGTCAGTC	TGTCTCTACG	ACTAGAATGG	AAAGCCTTAC	1020
TACTTCCTAT	GTATTCTTAA	TATTTCAAAT	GTCCTAATTA	TGTTTGGCTT	CTCTGTCTTT	1080
AAGGGATTTA	GTCTCTGGAT	TTGAAGAAAT	AAATAAATAA	ATAAAGGAAA	ACTAATTTTC	1140
TCGTGCCCGA	TGACTGCTAG	CTGAGCTCAG	GCCTACTGCA	TTCTACATTT	CGACTCTCTC	1200
CCTCTTCCCC	AGTGCTTTAG	CACTGGACTG	GGCAGTNCCT	GGCCTGGTCT	AACTCCTGTT	1260
TCCTGGTG GG	AATGTATAAT	AAGAACTCCA	TGAGTTCTGG	TATAAACACT	GTGGTCTGTG	1320
TGCTAATTAA	ATCTNGTGTT	TCCTACAGCC	CCTGACGAAA	AATGACTCAC	TGTGTAGTGT	1380
GAGGAGGTAC	GTGGTGAAGC	ATCGTACTGC	CCACAATGGG	ACGTGGTCAG	AAGATGTGGG	1440
AAATCGGACC	AATCTCACTT	TCCTGTGGAC	AGAACCAGCG	CACACTGTTA	CAGTTCTGGC	1500
TGTCAATTCC	CTCGGCGCTT	CCCTTGTGAA	TTTTAACCTT	ACCTTCTCAT	GGCCCATGAG	1560
TAAAGTGAGT	GCTGTGGAGT	CACTCAGTGC	TTATCCCCTG	AGCAGCAGCT	GTGTCATCCT	1620
TTCTTG GACA	CTGTCACCTG	ATGATTATAG	TCTGTTATAT	CTGGTTATTG	AATGGAAGAT	1680
CCTTAATGAA	GATGATGGAA	TGAAGTGGCT	TAGAATTCCC	TCGAATGTTA	AAAAGTTTTA	1740
TATCCACGAT	AATTTTATTC	CCATCGAGAA	ATATCAGTTT	AGTCTTTACC	CAGTATTTAT	1800
GGAAGGAGTT	GGAAAACCAA	AGATAATTAA	TGGTTTCACC	AAAGATGCTA	TCGACAAGCA	1860
GCAGAATGAC	GCAGGGCTGT	ATGTCATTGT	ACCCATAATT	ATTCCTCTT	GTGTCCTACT	1920
GCTCGGAACA	CTGTTAATTT	CACACCAGAG	AATGAAAAAG	TTGTTTTGGG	ACGATGTTCC	1980
AAACCCCAAG	AATTGTTCCCT	GGGCACAAGG	ACTGAATTTT	CAAAAGCCTG	AAACATTTGA	2040
GCATCTTTTT	ACCAAGCATG	CAGAATCAGT	GATATTTGGT	CCTCTTCTTC	TGGAGCCTGA	2100

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ACCCATTTCA GAAGAAATCA GTGTCGATAC AGCTTGGAAA AATAAAGATG AGATGGTCCC 2160
AGCAGCTATG GTCTCCCTTC TTTTGACCAC ACCAGACCCCT GAAAGCAGTT CTATTTGTAT 2220
TAGTGACCAG TGTAACAGTG CTAACTTCTC TGGGTCTCAG AGCACCCAGG TAACCTGTGA 2280
GGATGAGTGT CAGAGACAAC CCTCAGTTAA ATATGCAACT CTGGTCAGCA ACGATAAACT 2340
AGTGGAAACT GATGAAGAGC AAGGGTTTAT CCATAGTCCT GTCAGCAACT GCATCTCCAG 2400
TAATCATTC CCACTGAGGC AGTCTTTCTC TAGCAGCTCC TGGGAGACAG AGGCCAGAC 2460
ATTTTTCCTT TTATCAGACC AGCAACCCAC CATGATTTCA CCACAACCTT CATTCTCGGG 2520
GTTGGATGAG CTTTGGGAAC TGGAGGGAAG TTTTCCTGAA GAAAATCACA GGGAGAAGTC 2580
TGTCTGTTAT CTAGGAGTCA CCTCCGTCAA CAGAAGAGAG AGTGGTGTGC TTTTGACTGG 2640
TGAGGCAGGA ATCCTGTGCA CATTCCCAGC CCAGTGTCTG TTCAGTGACA TCAGGATCCT 2700
CCAGGAGAGA TGCTCACACT TTGTAGAAAA TAATTTGAGT TTAGGGACCT CTGGTGAGAA 2760
CTTTGTACCT TACATGCCCC AATTTCAAAC CTGTTCCACG CACAGTCACA AGATAATGGA 2820
GAATAAGATG TGTGACTTAA CTGTGTAATC TCATCCAAGA AGCCTCAAGG TTCCATTCCA 2880
GTAGAGCCTG TCATGTATAA TGTGTTCTTT ATTG 2914

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 499 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg Tyr Val Val
1           5           10           15
Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp Val Gly Asn
20        25        30
Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His Thr Val Thr
35        40        45
Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn Phe Asn Leu
50        55        60
Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu Ser Leu Ser

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65	70					75					80				
Ala Tyr Pro Leu Ser	Ser Ser Cys Val	Ile Leu Ser Trp Thr	Leu Ser												
	85						90						95		
Pro Asp Asp Tyr Ser	Leu Leu Tyr Leu	Val Ile Glu Trp Lys	Ile Leu												
	100						105						110		
Asn Glu Asp Asp Gly	Met Lys Trp Leu	Arg Ile Pro Ser	Asn Val	Lys											
	115						120						125		
Lys Phe Tyr Ile His	Asp Asn Phe Ile	Pro Ile Glu Lys	Tyr Gln	Phe											
	130						135						140		
Ser Leu Tyr Pro Val	Phe Met Glu Gly	Val Gly Lys Pro	Lys Ile	Ile											
	145						150						155		
Asn Gly Phe Thr Lys	Asp Ala Ile Asp	Lys Gln Gln Asn	Asp Ala	Gly											
	165						170						175		
Leu Tyr Val Ile Val	Pro Ile Ile Ile	Ser Ser Cys Val	Leu Leu	Leu											
	180						185						190		
Gly Thr Leu Leu Ile	Ser His Gln Arg	Met Lys Lys Leu	Phe Trp	Asp											
	195						200						205		
Asp Val Pro Asn Pro	Lys Asn Cys Ser	Trp Ala Gln Gly	Leu Asn	Phe											
	210						215						220		
Gln Lys Pro Glu Thr	Phe Glu His Leu	Phe Thr Lys His	Ala Glu	Ser											
	225						230						235		
Val Ile Phe Gly Pro	Leu Leu Leu Glu	Pro Glu Pro Ile	Ser Glu	Glu											
	245						250						255		
Ile Ser Val Asp Thr	Ala Trp Lys Asn	Lys Asp Glu Met	Val Pro	Ala											
	260						265						270		
Ala Met Val Ser Leu	Leu Leu Thr Thr	Pro Asp Pro Glu	Ser Ser	Ser											
	275						280						285		
Ile Cys Ile Ser Asp	Gln Cys Asn Ser	Ala Asn Phe Ser	Gly Ser	Gln											
	290						295						300		
Ser Thr Gln Val Thr	Cys Glu Asp Glu	Cys Gln Arg Gln	Pro Ser	Val											
	305						310						315		
Lys Tyr Ala Thr Leu	Val Ser Asn Asp	Lys Leu Val Glu	Thr Asp	Glu											
	325						330						335		
Glu Gln Gly Phe Ile	His Ser Pro Val	Ser Asn Cys Ile	Ser Ser	Asn											
	340						345						350		
His Ser Pro Leu Arg	Gln Ser Phe Ser	Ser Ser Ser Trp	Glu Thr	Glu											
	355						360						365		
Ala Gln Thr Phe Phe	Leu Leu Ser Asp	Gln Gln Pro Thr	Met Ile	Ser											
	370						375						380		
Pro Gln Leu Ser Phe	Ser Gly Leu Asp	Glu Leu Leu Glu	Leu Glu	Gly											
	385						390						395		
Ser Phe Pro Glu Glu	Asn His Arg Glu	Lys Ser Val Cys	Tyr Leu	Gly											
	405						410						415		

Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly Glu
 420 425 430

Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp Ile
 435 440 445

Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu Ser
 450 455 460

Leu Gly Thr Ser Gly Glu Asn Phe Val Pro Tyr Met Pro Gln Phe Gln
 465 470 475 480

Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys Asp
 485 490 495

Leu Thr Val

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 CODING REGION: 272-958
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACTCCT	180
GTTTCCTGGT GGGAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT	240
GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCAACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTTAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCAT	540
CCTTCCTGG AACTGTACAC CTGATGATTA TAGTCTGTTA TATCTGGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAATAAGTT	660
TTATATCCAC GATAATTTTA TTCCCATCGA GAAATATCAG TTAGTCTTT ACCCAGTATT	720

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TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA      780
GCAGCAGAAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTTCCT CTTGTGTCCT      840
ACTGCTCGGA ACACTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTTT GGGACGATGT      900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTTA      960
AGTATTTTAA CCCAGATATC TAAGGTTGCA GTTTAGATGC CACAGTACTT ACAGATCTTT     1020
AAACAACTTT AAAGGGCTTT ATGTTGTTGT GTTCATGTTT TCAAGCCTGT TCATCCTTTC     1080
TCTTTCTCAA AAGCTGGGTT TGGGATTTGA TCAGAGAAAA CAAAGTTCGC TCCCTTATCT     1140
CATGAGAGTT GACAACACAT CTATCTCTCT TTCTGCTTAC TGTACATAAA AAAAATAAAT     1200
ACTACAAGAG GAAGGAATGT TATAGATGGA GAATAGATAG                             1240

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg Tyr Val Val
1           5           10           15
Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp Val Gly Asn
20        25        30
Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His Thr Val Thr
35        40        45
Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn Phe Asn Leu
50        55        60
Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu Ser Leu Ser
65        70        75        80
Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp Thr Leu Ser
85        90        95
Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp Lys Ile Leu
100       105       110
Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser Asn Val Lys

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	115		120		125										
Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys	Tyr	Gln	Phe
	130					135					140				
Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro	Lys	Ile	Ile
145					150					155					160
Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn	Asp	Ala	Gly
				165					170					175	
Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val	Leu	Leu	Leu
			180					185					190		
Gly	Thr	Leu	Leu	Ile	Ser	His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp
		195					200					205			
Asp	Val	Pro	Asn	Pro	Lys	Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe
	210					215					220				
Gln	Lys	Val	Thr	Val											
225															

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2892 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
CODING REGION: 1-2700
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A8 (OB-Rd)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTTCCT	240
GAGTTATCCA AAACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AAACGTCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCCTC TGCCCCCACT GAAAGACAGC	540

TTTCAGACTG	TCCAATGCAA	CTGCAGTCTT	CGGGGATGTG	AATGTCATGT	GCCGGTACCC	600
AGAGCCAAAC	TCAACTACGC	TCTTCTGATG	TATTTGGAAA	TCACATCTGC	CGGTGTGAGT	660
TTTCAGTCAC	CTCTGATGTC	ACTGCAGCCC	ATGCTTGTTG	TGAAACCCGA	TCCACCCTTA	720
GGTTTGCATA	TGGAAGTCAC	AGATGATGGT	AATTTAAAGA	TTTCTTGGGA	CAGCCAAACA	780
ATGGCACCAT	TTCCGCTTCA	ATATCAGGTG	AAATATTTAG	AGAATTCTAC	AATTGTAAGA	840
GAGGCTGCTG	AAATTGTCTC	AGCTACATCT	CTGCTGGTAG	ACAGTGTGCT	TCCTGGATCT	900
TCATATGAGG	TCCAGGTGAG	GAGCAAGAGA	CTGGATGGTT	CAGGAGTCTG	GAGTGACTGG	960
AGTTCACCTC	AAGTCTTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTGGAT	CGAATGCTTC	TTTTCATTCG	ATCTACAAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTTGGTG	GAGGAATCTA	GCTGAGAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAACCTGCGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCCTT	AGGTTCACTT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAAGTGAAA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTGAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTTCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCTGTGGA	CAGAACCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTCATCC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGA	TAATTTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTTAC	CCAGTATTTA	TGGAAGGAGT	TGGA AAAACCA	2460
AAGATAATTA	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520

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TATGTCATTG TACCCATAAT TATTTCTCT TGTGTCCTAC TGCTCGGAAC ACTGTTAATT 2580
TCACACCAGA GAATGAAAAA GTTGTTTTGG GACGATGTTT CAAACCCCAA GAATTGTTCC 2640
TGGGCACAAG GACTGAATTT CCAAAGGAT ATATCTTTAC ATGAAGTTTT TATTTTCAGA 2700
TAGCCTCTGG CAGATTCTCA CTGTGGCCTG AGGCAGCCTG AAACATTTGA GCATCTTTTT 2760
ACCAAGCATG CAGAATCAGT GATATTTGGT CCTCTTCTTC TGGAGCCTGA ACCCATTTCA 2820
GAAGAAATCA GTGTCGATAC AGCTTGAAA AATAAAGATG AGATGGTCCC AGCAGCTATG 2880
GTCTCCCTTC TT 2892

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 900 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu
1          5          10
Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys
20        25        30
Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu
35        40        45
Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser
50        55        60
Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro
65        70        75        80
Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly
85        90        95
Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala
100       105       110
Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
115       120       125
Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
130       135       140

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Glu 145	Pro	Leu	Pro	Lys	Asn 150	Pro	Phe	Lys	Asn	Tyr 155	Asp	Ser	Lys	Val	His 160
Leu	Leu	Tyr	Asp	Leu 165	Pro	Glu	Val	Ile	Asp 170	Asp	Ser	Pro	Leu	Pro 175	Pro
Leu	Lys	Asp	Ser 180	Phe	Gln	Thr	Val	Gln 185	Cys	Asn	Cys	Ser	Leu 190	Arg	Gly
Cys	Glu	Cys 195	His	Val	Pro	Val	Pro 200	Arg	Ala	Lys	Leu	Asn 205	Tyr	Ala	Leu
Leu	Met 210	Tyr	Leu	Glu	Ile	Thr 215	Ser	Ala	Gly	Val	Ser 220	Phe	Gln	Ser	Pro
Leu 225	Met	Ser	Leu	Gln 230	Pro	Met	Leu	Val	Val	Lys 235	Pro	Asp	Pro	Pro	Leu 240
Gly	Leu	His	Met	Glu 245	Val	Thr	Asp	Asp	Gly 250	Asn	Leu	Lys	Ile	Ser 255	Trp
Asp	Ser	Gln	Thr 260	Met	Ala	Pro	Phe	Pro 265	Leu	Gln	Tyr	Gln	Val 270	Lys	Tyr
Leu	Glu 275	Asn	Ser	Thr	Ile	Val	Arg 280	Glu	Ala	Ala	Glu	Ile 285	Val	Ser	Ala
Thr 290	Ser	Leu	Leu	Val	Asp	Ser 295	Val	Leu	Pro	Gly	Ser 300	Ser	Tyr	Glu	Val
Gln 305	Val	Arg	Ser	Lys	Arg 310	Leu	Asp	Gly	Ser	Gly 315	Val	Trp	Ser	Asp	Trp 320
Ser	Ser	Pro	Gln 325	Val	Phe	Thr	Thr	Gln	Asp 330	Val	Val	Tyr	Phe	Pro 335	Pro
Lys	Ile	Leu	Thr 340	Ser	Val	Gly	Ser	Asn 345	Ala	Ser	Phe	His	Cys 350	Ile	Tyr
Lys	Asn 355	Glu	Asn	Gln	Ile	Ile	Ser 360	Ser	Lys	Gln	Ile	Val 365	Trp	Trp	Arg
Asn 370	Leu	Ala	Glu	Lys	Ile	Pro 375	Glu	Ile	Gln	Tyr	Ser 380	Ile	Val	Ser	Asp
Arg 385	Val	Ser	Lys	Val	Thr 390	Phe	Ser	Asn	Leu	Lys 395	Ala	Thr	Arg	Pro	Arg 400
Gly	Lys	Phe	Thr 405	Tyr	Asp	Ala	Val	Tyr	Cys 410	Cys	Asn	Glu	Gln	Ala 415	Cys
His	His	Arg	Tyr 420	Ala	Glu	Leu	Tyr	Val 425	Ile	Asp	Val	Asn 430	Ile	Asn	Ile
Ser	Cys	Glu 435	Thr	Asp	Gly	Tyr	Leu 440	Thr	Lys	Met	Thr	Cys 445	Arg	Trp	Ser
Pro	Ser 450	Thr	Ile	Gln	Ser	Leu	Val 455	Gly	Ser	Thr	Val 460	Gln	Leu	Arg	Tyr
His 465	Arg	Arg	Ser	Leu	Tyr 470	Cys	Pro	Asp	Ser	Pro 475	Ser	Ile	His	Pro	Thr 480
Ser	Glu	Pro	Lys	Asn 485	Cys	Val	Leu	Gln	Arg 490	Asp	Gly	Phe	Tyr	Glu 495	Cys

Val	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg		
			500					505					510				
Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu		
		515					520					525					
Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu		
	530					535					540						
Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val		
545					550					555					560		
Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly		
				565					570					575			
Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys		
			580					585					590				
Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln		
		595					600					605					
Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser		
	610					615					620						
Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly		
625					630					635					640		
Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg		
				645					650					655			
Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys		
			660					665					670				
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr		
		675					680					685					
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr		
	690					695				700							
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala		
705					710					715					720		
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val		
				725					730					735			
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val		
			740					745					750				
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu		
		755					760						765				
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu		
						775					780						
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile		
785					790					795					800		
Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly		
				805					810					815			
Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp		
			820					825					830				
Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile		
		835					840					845					

Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
850 855 860

Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
865 870 875 880

Trp Ala Gln Gly Leu Asn Phe Gln Lys Asp Ile Ser Leu His Glu Val
885 890 895

Phe Ile Phe Arg
900

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
CODING REGION: 1-2415
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A20 (OB-Re)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGATGTGTC AGAAATTCTA TGTGGTTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACTTAACC TGGCATATCC AATCTCTCCC TGGAAATTTA AGTTGTTTTG TGGACCACCG	120
AACACAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTTG	180
AAGGGGGCTT CTGAAGCAAT TGTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTTCT	240
GAGTTATCCA AACAGTCTT CCACTGTTGC TTTGGGAATG AGCAAGGTCA AACTTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATTC	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCGCTC TGCCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTTG TGAAACCCGA TCCACCCTTA	720
GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTTGGA CAGCCAAACA	780
ATGGCACCAT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960

AGTTCACCTC	AAGTCTTTAC	CACACAAGAT	GTTGTGTATT	TTCCACCCAA	AATTCTGACT	1020
AGTGTGGAT	CGAATGCTTC	TTTTATTGC	ATCTACAAA	ACGAAAACCA	GATTATCTCC	1080
TCAAAACAGA	TAGTTTGGTG	GAGGAATCTA	GCTGAGAAAA	TCCCTGAGAT	ACAGTACAGC	1140
ATTGTGAGTG	ACCGAGTTAG	CAAAGTTACC	TTCTCCAACC	TGAAAAGCCAC	CAGACCTCGA	1200
GGGAAGTTTA	CCTATGACGC	AGTGTACTGC	TGCAATGAGC	AGGCGTGCCA	TCACCGCTAT	1260
GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCATCTAT	TCATCCTACG	1440
TCTGAGCCCA	AAAACGCGT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GACTCGCCAC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACCACTACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTTGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGAAA	AGAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTGAGAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTTCG	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TAAAAGTTCC	TATGAGAGGG	1920
CCTGAATTTT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCTGTGGA	CAGAACCAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATTC	CCTCGGCGCT	2160
TCCCTTGGA	ATTTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGTCATCC	TTTCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTTT	ATATCCACGG	TATGTGTACT	2400
GTACTTTTCA	TGGATTAGTA	TGACACTGTA	GACTGGCAAT	TCTGATAATA	AATCATTTAA	2460
TGACAACC						2468

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu	1	5	10	15
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys	20	25	30	
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu	35	40	45	
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser	50	55	60	
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro	65	70	75	80
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly	85	90	95	
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	100	105	110	
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	115	120	125	
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	130	135	140	
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	145	150	155	160
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro	165	170	175	
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly	180	185	190	
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu	195	200	205	
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro	210	215	220	
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu	225	230	235	240
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp	245	250	255	
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr	260	265	270	
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala	275	280	285	

Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val
	290					295					300				
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp
305					310					315					320
Ser	Ser	Pro	Gln	Val	Phe	Thr	Thr	Gln	Asp	Val	Val	Tyr	Phe	Pro	Pro
				325					330					335	
Lys	Ile	Leu	Thr	Ser	Val	Gly	Ser	Asn	Ala	Ser	Phe	His	Cys	Ile	Tyr
			340					345					350		
Lys	Asn	Glu	Asn	Gln	Ile	Ile	Ser	Ser	Lys	Gln	Ile	Val	Trp	Trp	Arg
		355					360					365			
Asn	Leu	Ala	Glu	Lys	Ile	Pro	Glu	Ile	Gln	Tyr	Ser	Ile	Val	Ser	Asp
	370					375					380				
Arg	Val	Ser	Lys	Val	Thr	Phe	Ser	Asn	Leu	Lys	Ala	Thr	Arg	Pro	Arg
385					390					395					400
Gly	Lys	Phe	Thr	Tyr	Asp	Ala	Val	Tyr	Cys	Cys	Asn	Glu	Gln	Ala	Cys
				405					410					415	
His	His	Arg	Tyr	Ala	Glu	Leu	Tyr	Val	Ile	Asp	Val	Asn	Ile	Asn	Ile
			420					425					430		
Ser	Cys	Glu	Thr	Asp	Gly	Tyr	Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser
		435				440						445			
Pro	Ser	Thr	Ile	Gln	Ser	Leu	Val	Gly	Ser	Thr	Val	Gln	Leu	Arg	Tyr
	450					455					460				
His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
465					470					475					480
Ser	Glu	Pro	Lys	Asn	Cys	Val	Leu	Gln	Arg	Asp	Gly	Phe	Tyr	Glu	Cys
				485					490					495	
Val	Phe	Gln	Pro	Ile	Phe	Leu	Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg
			500					505					510		
Ile	Asn	His	Ser	Leu	Gly	Ser	Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu
		515					520					525			
Pro	Asp	Ser	Val	Val	Lys	Pro	Leu	Pro	Pro	Ser	Asn	Val	Lys	Ala	Glu
	530					535					540				
Ile	Thr	Val	Asn	Thr	Gly	Leu	Leu	Lys	Val	Ser	Trp	Glu	Lys	Pro	Val
545					550					555					560
Phe	Pro	Glu	Asn	Asn	Leu	Gln	Phe	Gln	Ile	Arg	Tyr	Gly	Leu	Ser	Gly
				565					570					575	
Lys	Glu	Ile	Gln	Trp	Lys	Thr	His	Glu	Val	Phe	Asp	Ala	Lys	Ser	Lys
			580					585					590		
Ser	Ala	Ser	Leu	Leu	Val	Ser	Asp	Leu	Cys	Ala	Val	Tyr	Val	Val	Gln
		595					600					605			
Val	Arg	Cys	Arg	Arg	Leu	Asp	Gly	Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser
	610					615					620				
Ser	Pro	Ala	Tyr	Thr	Leu	Val	Met	Asp	Val	Lys	Val	Pro	Met	Arg	Gly
625					630					635					640

Pro	Glu	Phe	Trp	Arg	Lys	Met	Asp	Gly	Asp	Val	Thr	Lys	Lys	Glu	Arg	
				645					650					655		
Asn	Val	Thr	Leu	Leu	Trp	Lys	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	
			660					665					670			
Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	
		675					680					685				
Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	
	690					695					700					
Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	
705					710					715					720	
Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	
				725					730					735		
Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	
			740					745					750			
Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	
		755					760					765				
Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	
	770					775					780					
Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Gly	Met	Cys	Thr	
785					790					795					800	
Val	Leu	Phe	Met	Asp												
				805												

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn	Phe	Gln	Lys	Arg	Thr	Asp	Leu
1				5			

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn 1	Phe	Gln	Lys	Pro 5	Glu	Thr	Phe	Glu	Gln 10	Leu	Phe	Thr	Lys	His 15	Ala
Glu	Ser	Val	Ile 20	Phe	Gly	Pro	Leu	Leu 25	Leu	Glu	Pro	Glu	Pro 30	Ile	Ser
Glu	Glu	Ile 35	Ser	Val	Asp	Thr	Ala 40	Trp	Lys	Asn	Lys	Asp 45	Glu	Met	Val
Pro	Ala 50	Ala	Met	Val	Ser	Leu 55	Leu	Trp	Thr	Thr	Pro 60	Asp	Pro	Glu	Ser
Ser 65	Ser	Ile	Cys	Ile	Ser 70	Asp	Gln	Cys	Asn	Ser 75	Ala	Asn	Phe	Ser	Gly 80
Ser	Gln	Ser	Thr	Gln 85	Val	Cys	Glu	Asp	Glu 90	Cys	Gln	Arg	Gln	Pro 95	Ser
Val	Lys	Tyr	Ala 100	Thr	Leu	Val	Ser	Asn 105	Asp	Lys	Leu	Val	Glu 110	Thr	Asp
Glu	Glu	Gln 115	Gly	Phe	Ile	His	Ser 120	Pro	Val	Ser	Asn	Cys 125	Ile	Ser	Ser
Asn	His 130	Ser	Pro	Leu	Arg	Gln 135	Ser	Phe	Ser	Ser	Ser 140	Ser	Trp	Glu	Thr
Glu 145	Ala	Gln	Thr	Phe	Phe 150	Leu	Leu	Ser	Asp	Gln 155	Gln	Pro	Thr	Met	Ile 160
Ser	Pro	Gln	Leu	Ser 165	Phe	Ser	Gly	Leu	Asp 170	Glu	Leu	Leu	Glu	Leu 175	Glu
Gly	Ser	Phe	Pro 180	Glu	Glu	Asn	His	Arg 185	Glu	Lys	Ser	Val	Cys 190	Tyr	Leu
Gly	Val	Thr 195	Ser	Val	Asn	Arg	Arg 200	Glu	Ser	Gly	Val	Leu 205	Leu	Thr	Gly
Glu	Ala 210	Gly	Ile	Leu	Cys	Thr 215	Phe	Pro	Ala	Gln	Cys 220	Leu	Phe	Ser	Asp
Ile 225	Arg	Ile	Leu	Gln	Glu 230	Arg	Cys	Ser	His	Phe 235	Val	Glu	Asn	Asn	Leu 240
Ser	Leu	Gly	Thr	Ser 245	Gly	Glu	Asn	Phe	Gly 250	Pro	Tyr	Met	Pro	Gln 255	Phe

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- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal

- (vii) IMMEDIATE SOURCE:
- (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe	Tyr	Ile	His	Gly	Met	Cys	Thr	Val	Leu	Phe	Met	Asp
1				5					10			

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro	Gln	Lys	Arg	Thr	Asp	Thr	Leu
1				5			

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

12

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTAA TTTACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACC CTTGCTCTTC A

21

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAC AACATAAAGC CC

22

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
1				5					10					15	
Ser Glu Pro Lys															
20															

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn
1				5					10					15	
Cys Ser Trp															

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

23

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

27

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: not relevant

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys
1 5 10

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG CCGAGGGAAT TGACAGCCAG AACTGTAACA GTGTGCGCTG GTTCTGTCCA	60
CAGGAAAGTG AGATTGGTCC GATTTCCCAC ATCTTCTGAC CACGTCCCAT TGTGGGCAGT	120
ACGATGCTTC ACCACGTACC TCCTCACACT ACACAGTGAG TCATTT	166

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCC ACAATGGGAC GTGGTCAGAA GATGTGGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG AACCAGCGCA CACTGTTACA GTTCTGGCTG TCAATTCCT	120
CGGCGCTTCC CTTGTGAATT TTAACCTTAC CTTCTCATGG CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT ATCCCCTGAG CAGCAGCTGT GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC TGTTATATCT GGTTATTGAA TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA	320

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG CTGACAGGAC TATGGATAAA CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG ACCAGAGTTG CATATTTAAC TGAGGGTGT CTCTGACACT	120
CATCCTCACA GGTTACCTGG GTGCTCTGAG ACCCAGAG	158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAGGCTC TGTGTTTCATT TGATGTTTCAG	60
AAGTCAGCAA GGTTCCTCATA TGTCCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG	120
CTAACAAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA AACTACTTGT GTGTTTTTACT	180
TAAAGATACG AG	192

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTTTC TCATCTAACA AGCAAGCAAA GGAAGTCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA	168

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATCTTTTAT ATGATCTGCC TGAAGTCATA GATGATTCGC	60
CTCTGCCCCC ACTGAAAGAC AGNTTTCAGA CTGTCCAATG NAACTGCAGT CTTTCGGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTTCTG ATGTATTTGG	180
NAATCACATC TGCCGGTGTG AGTTTTTCAGT CACCTCTGAT GTCAGTGCAG CCCATGCTTG	240
TTGTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTTCAACAAT TGGTTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACCTTA AATTTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA	180

AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTCAG 240
AACGATTCCT 250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC 18

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG 22

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

X

(D) OLOGYlinear

(ii) MOLECULETYPE:cDNA

(iii) HYPOTHETICALNO

(iv) ANTI-SENSENO

(xi) SEQUENCEDESCRIPTIONSEQ ID NO:47:

AGAGAGATCCTGACCCTAFT

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTCCTTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATTCGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCCTG

sub C2
cont.